Amendments to the Claims:

The following Listing of Claims will replace all prior versions, and listings, of the claims in the above-identified application.

Listing of Claims

1. (currently amended) An isolated and purified-poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) or a functional equivalent thereof which is at least 95% ~~85%~~ homologous to human PARP2 (SEQ ID NO: 2) ~~thereto~~, exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

   a) has a functional NAD^+ binding domain comprising the sequence ~~motif~~ $PX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:11)
   in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

   and

   b) lacks a zinc finger sequence ~~motif~~ of the formula $CX_2CX_mHX_2C$ (SEQ ID NO:30)
   in which m is an integral value of 28 or 30, and the X radicals are, independently of one another, any amino acid.

2. (currently amended) The PARP homolog as claimed in claim 1, wherein the functional NAD^+ binding domain comprises the following sequence ~~motif~~:
   $(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:12)
   in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid.

3. (currently amended) The PARP homolog as claimed in claim 1, further comprising the [[part-]] sequence ~~motif~~:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)

in which the X radicals are, independently of one another, any amino acid.

4-32. (canceled)

33. (currently amended) The PARP homolog as claimed in claim 1, wherein the functional NAD^+ binding domain comprises the following sequence ~~motif~~:

$LLWHG(S/T)X_7IL(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFAX_3SKSAXY$ (SEQ ID NO:13)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

34. (currently amended) The PARP homolog as claimed in claim 1, further comprising [[part-]] sequence: ~~motif~~

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16)

in which the X radicals are, independently of one another, any amino acid.

35. (currently amended) The PARP homolog as claimed in claim 1, further comprising [[part-]] sequence: ~~motif~~

$XL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17)

in which the X radicals are, independently of one another, any amino acid.

36. (currently amended) The PARP homolog as claimed in claim 1, further comprising [[part-]] sequence: ~~motif~~

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18)

in which the X radicals are, independently of one another, any amino acid.

37. (currently amended) The PARP homolog as claimed in claim 1, further comprising

[[part-]] sequence: ~~motif~~

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

38. (currently amended) An isolated poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) or a functional equivalent thereof which is at least 95% ~~85%~~ homologous to human PARP2 (SEQ ID NO: 2) ~~thereto~~, exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

a) has a functional NAD^+ binding domain comprising the sequence ~~motif~~

$PX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:11)

in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

and

b) lacks a zinc finger sequence ~~motif~~ of the formula

$CX_2CX_mHX_2C$ (SEQ ID NO:30)

in which m is an integral value of 28 or 30, and the X radicals are, independently of one another, any amino acid

further comprising a leucine zipper-like sequence ~~motif~~:

$(L/V)X_6LX_6LX_6L$ (SEQ ID NO: 14)

wherein X radicals are, independently of one another, any amino acid.

39. (currently amended) The PARP homolog as claimed in claim 38, further comprising at least one of the following [[part-]] sequences ~~motifs~~:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15),

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

40. (currently amended) The PARP homolog as claimed in claim 38, further comprising [[part-]] sequences ~~motifs~~:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

41. (currently amended) The PARP homolog as claimed in claim 38, further comprising [[part-]] sequences ~~motifs~~:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO:15)

is closest to the N terminus.

42. (currently amended) The PARP homolog as claimed in claim 1, further comprising [[part-]] sequences ~~motifs~~:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

43. (currently amended) The PARP homolog as claimed in claim 1, further comprising [[part-]] sequences ~~motifs~~:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

FYTXIPHXFGX_3PP (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO:15)

is closest to the N terminus.

44. (currently amended) The PARP homolog as claimed in claim 1, further comprising at least one of the following:

$GX_3LXEVALG$ (SEQ ID NO: 20),

GX2S$X_4GX_3PX_aLXGX_2V$ (SEQ ID NO: 21), and

$E(Y/F)X_2YXYX_3QXYLL$ (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

45. (currently amended) The PARP homolog as claimed in claim 1, further comprising

$GX_3LXEVALG$ (SEQ ID NO: 20),

$GX_2SX_4GX_3PX_aLXGX_2V$ (SEQ ID NO: 21), and

$E(Y/F)X_2YX_3QX_4YLL$ (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

46. (currently amended) The PARP homolog as claimed in claim 1, further comprising

$GX_3LXEVALG$ (SEQ ID NO: 20),

$GX_2SX_4GX_3PX_aLXGX_2V$ (SEQ ID NO: 21), and

$E(Y/F)X_2YX_3QX_4YLL$ (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid, wherein

$E(Y/F)X_2YX_3QX_4YLL$ (SEQ ID NO: 22)

is closest to the C terminus.

47. (currently amended) An isolated poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) or a functional equivalent thereof which is at least 95% ~~85%~~ homologous to human PARP2 (SEQ ID NO: 2) ~~thereto~~, exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

a) has a functional NAD^+ binding domain comprising the sequence ~~motif~~ $PX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:11)

in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

and

b) lacks a zinc finger sequence.

48. (currently amended) The PARP homolog as claimed in claim 47, wherein said PARP lacks a zinc finger sequence ~~motif~~ of the formula

$CX_2CX_mHX_2C$ (SEQ ID NO:30)

in which m is an integral value of 28 or 30, and

the X radicals are, independently of one another, any amino acid.

49. (currently amended) The PARP homolog as claimed in claim 47, wherein the functional

NAD^+ binding domain comprises the following sequence ~~motif~~:

(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFA (SEQ ID NO:12)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

50. (currently amended) The PARP homolog as claimed in claim 47, wherein the functional NAD^+ binding domain comprises the following sequence ~~motif~~:

LLWHG(S/T)X_7IL(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFAX_3SKSAXY (SEQ ID NO:13)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

51. (currently amended) The PARP homolog as claimed in claim 47, further comprising a leucine zipper-like sequence:

(L/V)X_6LX_6LX_6L (SEQ ID NO: 14)

wherein X radicals are, independently of one another, any amino acid.

52. (currently amended) The PARP homolog as claimed in claim 51, further comprising at least one of the following [[part-]] sequences ~~motifs~~:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15),

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

53. (currently amended) The PARP homolog as claimed in claim 51, further comprising:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15),

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

54. (currently amended) The PARP homolog as claimed in claim 51, further comprising:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15),

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)

is closest to the N terminus.

55. (currently amended) The PARP homolog as claimed in claim 47, further comprising at least one of the following:

$GX_3LXEVALG$ (SEQ ID NO: 20),

$GX_2SX_4GX_3PX_aLXGX_2V$ (SEQ ID NO: 21), and

$E(Y/F)X_2YX_3QX_4YLL$ (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

56. (currently amended) The PARP homolog as claimed in claim 47, further comprising

$GX_3LXEVALG$ (SEQ ID NO: 20),

$GX_2SX_4GX_3PX_aLXGX_2V$ (SEQ ID NO: 21), and

$E(Y/F)X_2YX_3QX_4YLL$ (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

57. (currently amended) The PARP homolog as claimed in claim 47, further comprising

$GX_3LXEVALG$ (SEQ ID NO: 20),

$GX_2SX_4GX_3PX_aLXGX_2V$ (SEQ ID NO: 21), and

$E(Y/F)X_2YX_3QX_4YLL$ (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid, wherein

$E(Y/F)X_2YX_3QX_4YLL$ (SEQ ID NO: 22)

is closest to the C terminus.

58. (currently amended) The PARP homolog as claimed in claim 51, further comprising at least one of the following:

$GX_3LXVALG$ (SEQ ID NO: 20),

$GX2SX_4GX_3PX_aLXGX_2V$ (SEQ ID NO: 21), and

$E(Y/F)X_2YX_3QX_4YLL$ (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

59. (currently amended) The PARP homolog as claimed in claim 51, further comprising

$GX_3LXEVALG$ (SEQ ID NO: 20),

$GX_2SX_4GX_3PX_aLXGX_2V$ (SEQ ID NO: 21), and

$E(Y/F)X_2YX_3QX_4YLL$ (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

60. (currently amended) The PARP homolog as claimed in claim 51, further comprising

$GX_3LXEVALG$ (SEQ ID NO: 20),

$GX_2SX_4GX_3PX_aLXGX_2V$ (SEQ ID NO: 21), and

$E(Y/F)X_2YX_3QX_4YLL$ (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid, wherein

$E(Y/F)X_2YX_3QX_4YLL$ (SEQ ID NO: 22

is closest to the C terminus.